

CLAIMS

1. An isolated human protein having an amino acid sequence which is at least 85% identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

2. The isolated human protein of claim 1 which has an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2.

3. A fusion protein comprising a first protein segment and a second protein segment fused together by means of a peptide bond, wherein the first protein segment consists of a protein having an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2.

4. A preparation of antibodies which specifically bind to a protein having an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2.

5. A cDNA molecule which encodes a protein having an amino acid sequence which is at least 85% identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

6. The cDNA molecule of claim 5 which encodes an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2.

7. The cDNA molecule of claim 6 which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:6 and 7.

8. A cDNA molecule which is at least 85% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOS:6 and 7, wherein percent identity is determined using a Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1.

9. An isolated and purified subgenomic polynucleotide comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS:6 and 7 after washing with 0.2X SSC at 65 °C, wherein the nucleotide sequence encodes a protein having an amino acid sequence

selected from the group consisting of SEQ ID NOS:1 and 2.

10. A construct comprising:

a promoter; and

a polynucleotide segment encoding an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2, wherein the polynucleotide segment is located downstream from the promoter, wherein transcription of the polynucleotide segment initiates at the promoter.

11. A host cell comprising a construct which comprises:

a promoter; and

a polynucleotide segment encoding an amino acid sequence selected from the group consisting of SEQ ID NOS:1 and 2.

12. A recombinant host cell comprising a new transcription initiation unit, wherein the new transcription initiation unit comprises in 5' to 3' order:

(a) an exogenous regulatory sequence;

(b) an exogenous exon; and

(c) a splice donor site, wherein the new transcription initiation unit is located upstream of a coding sequence of a gene, wherein the coding sequence is selected from the group consisting of SEQ ID NOS:6 and 7, wherein the exogenous regulatory sequence controls transcription of the coding sequence of the gene.

13. A method of screening for a compound capable of modulating cell death inducing activity of a protein, comprising the steps of:

incubating a first population of cells and a protein in the presence of a test compound, wherein the protein comprises an amino acid sequence selected from the group of amino acid sequences shown in SEQ ID NOS:1-5;

incubating a second population of cells and the protein in the absence of a test compound; and

determining viability of the first and second populations, wherein a test compound which increases or decreases viability of the first population relative to the second population is identified as capable of modulating the cell death inducing activity of the protein.

14. The method of claim 13 wherein the protein is provided to the first and

second populations of cells by transfecting the first and second populations of cells with a polynucleotide encoding the protein.

15. The method of claim 13 wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:6-10.

5 16. A method of identifying a binding partner of a first protein, comprising the steps of:

incubating a first protein with a second protein, wherein the first protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 1-5;

10 detecting formation of a complex between the first and second proteins, wherein formation of the complex identifies the second protein as a binding partner of the first protein.

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